IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICANTS:	**Sohocki, M., et.al.**	§	ART UNIT NO.:**1645**
SERIAL NO.:	**09/765,061**	§	EXAMINER: **FRIEND, THF**
FILED:	**01/17/01**	§	DOCKET NO.:**25630/16UTL**
		§	
TITLE:	**Mutations in a Novel**	§	
Photoreceptor-Pineal Gene on 17p		§	
Cause Leber Congenital Amaurosi (LCA4)		§	

EV 328 518 805 US	**CERTIFICATE OF MAIL BY EXPRESS MAIL**	June 6, 2003
Express Mail Number		Date of Deposit

I hereby certify that this paper or fee is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 C.F.R. § 1.10 on the date indicated above and is addressed to the:

Commissioner of Patent
MS SEQUENCE
P.O. Box, Alexandria, VA 22313-1450

Robert W. Strozier — June 6, 2003 (Date of Signature)

STATEMENT REGARDING SUBSTITUTE PAPER COPY OF SEQUENCE LISTING AND CRF COPY OF SEQUENCE LISTING

Dear Sir/Madam:

In response to a 6 June 2003Notice to Comply with Sequence Rules, Applicant used the PatentIn 3.2 software for the United States Patent and Trademark Office to generate a hard copy and an identical electronic copy of the sequences listed on Page 49, Table 1 of the application as filed. The sequence listing was also checked using Checker 3.0, with no errors reported, except that the sequences are number from 79-88 so that the sequences can append to the previously submitted sequences 1-78.

Applicant hereby asserts that the hard copy and electronic copy are identical. Please note that an electronic copy of the Checker Report is also on the diskette.

Respectfully submitted,

Date: **June 6, 2003**

Robert W. Strozier, Reg. No. 34,024
Attorney for Applicants

Application No.: 09/765,061

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- [ ] 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- [ ] 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- [ ] 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- [X] 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- [ ] 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- [ ] 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- [ ] 7. Other: _____

RECEIVED
JUN 11 2003
TECH CENTER 1600/2900

Applicant Must Provide:

- [X] An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- [X] An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- [X] A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

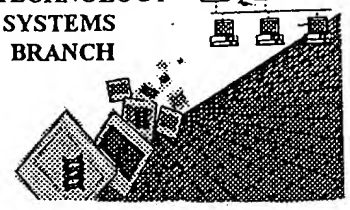
For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support
Technical Assistance.....703-~~287-0200~~ 684 1125
To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

C3 1600

BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/765,061C
Source: OIPE
Date Processed by STIC: 1/7/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
   Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

C IPE

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/765,061C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ✓	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2 ____	Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3 ____	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4 ____	Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5 ____	Variable Length	Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6 ____	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7 ____	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8 ____	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9 ____	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10 ____	Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11 ____	Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12 ____	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13 ____	Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

Does Not Comply
Corrected Pages Needed

RAW SEQUENCE LISTING DATE: 01/07/2003
PATENT APPLICATION: **US/09/765,061C** TIME: 14:04:21

Input Set : **A:\SQ 09765061.txt**
Output Set: **N:\CRF4\01072003\I765061C.raw**

```
      3 <110> APPLICANT: The Board of Regents of the University of Texas System
      5 <120> TITLE OF INVENTION: MUTATIONS IN A NOVEL PHOTORECEPTOR-PINEAL GENE ON 17P
      6       CAUSE LEBER CONGENITAL AMAUROSIS (LCA4)
      8 <130> FILE REFERENCE: 96606/16UTL
     10 <140> CURRENT APPLICATION NUMBER: 09/765,061C
C--> 11 <141> CURRENT FILING DATE: 2003-01-07
     13 <150> PRIOR APPLICATION NUMBER: 60/331362
     14 <151> PRIOR FILING DATE: 2001-01-04
     16 <160> NUMBER OF SEQ ID NOS: 10 — but seq. nos. were designated as 79 through 88
     18 <170> SOFTWARE: PatentIn version 3.1


ERRORED SEQUENCES

     20 <210> SEQ ID NO: 79
     21 <211> LENGTH: 34
     22 <212> TYPE: DNA
     23 <213> ORGANISM: Homo sapiens
     25 <220> FEATURE:
     26 <221> NAME/KEY: exon
     27 <222> LOCATION: (1)..(34)
     28 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence
     29       and Resi
     30       dues 11-34 are the intronic sequence
     33 <400> SEQUENCE: 79
E--> 34 cgg atc ccg agt gag tgg ggc cct ccg gag cag a
     35    34
     38 <210> SEQ ID NO: 80
     39 <211> LENGTH: 35
     40 <212> TYPE: DNA
     41 <213> ORGANISM: Homo sapiens
     43 <220> FEATURE:
     44 <221> NAME/KEY: exon
     45 <222> LOCATION: (1)..(35)
     46 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic
     47       sequence an
     48       d Residues 26-35 are the exonic sequence.
     51 <400> SEQUENCE: 80
E--> 52 cag agt gca ccg tct cgg tga cta ggt gat ctt tc
     53    35
     56 <210> SEQ ID NO: 81
     57 <211> LENGTH: 35
     58 <212> TYPE: DNA
```

nucleotides must be in groups of 10 lines with enumeration on the right margin — per § 1.822(c)(2)+(6) of the Rules

-if wrapped nucleic, see error summary sheet item 1

RAW SEQUENCE LISTING DATE: 01/07/2003
PATENT APPLICATION: **US/09/765,061C** TIME: 14:04:21

Input Set : **A:\SQ 09765061.txt**
Output Set: **N:\CRF4\01072003\I765061C.raw**

```
     59 <213> ORGANISM: Homo sapiens
     61 <220> FEATURE:
     62 <221> NAME/KEY: exon
     63 <222> LOCATION: (1)..(35)
     64 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence
     65       and Resi
     66       dues 11-35 are the intronic sequence
     69 <400> SEQUENCE: 81
E--> 70 csa cac cat cgt aag tag gcc ctg cgc gcc tgt ct
     71    35
     74 <210> SEQ ID NO: 82
     75 <211> LENGTH: 35
     76 <212> TYPE: DNA
     77 <213> ORGANISM: Homo sapiens
     79 <220> FEATURE:
     80 <221> NAME/KEY: exon
     81 <222> LOCATION: (1)..(35)
     82 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic
     83       sequence an
     84       d Residues 26-35 are the exonic sequence.
     87 <400> SEQUENCE: 82
E--> 88 gcc atc cat ccg ttt atc ccc aca gca cac ggg gg
     89    35
     92 <210> SEQ ID NO: 83
     93 <211> LENGTH: 35
     94 <212> TYPE: DNA
     95 <213> ORGANISM: Homo sapiens
     97 <220> FEATURE:
     98 <221> NAME/KEY: exon
     99 <222> LOCATION: (1)..(35)
    100 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence
    101       and Resi
    102       dues 11-35 are the intronic sequence
    105 <400> SEQUENCE: 83
E--> 106 gct gct gca ggt ggg gct ggg gtt ggc agg gct gg
    107    35
    110 <210> SEQ ID NO: 84
    111 <211> LENGTH: 35
    112 <212> TYPE: DNA
    113 <213> ORGANISM: Homo sapiens
    115 <220> FEATURE:
    116 <221> NAME/KEY: exon
    117 <222> LOCATION: (1)..(35)
    118 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic
    119       sequence an
    120       d Residues 26-35 are the exonic sequence.
    123 <400> SEQUENCE: 84
E--> 124 cac tga cct gca gct ctg ggg cca ggt tga tgc cc
    125    35
```

RAW SEQUENCE LISTING DATE: 01/07/2003
PATENT APPLICATION: US/09/765,061C TIME: 14:04:21

Input Set : A:\SQ 09765061.txt
Output Set: N:\CRF4\01072003\I765061C.raw

<210> SEQ ID NO: 85
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: exon
<222> LOCATION: (1)..(35)
<223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence and Resi dues 11-35 are the intronic sequence
<400> SEQUENCE: 85
E--> **gca gac caa ggt cag agg ccg ctg gcc acg ggg tg**
35
<210> SEQ ID NO: 86
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: exon
<222> LOCATION: (1)..(35)
<223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic sequence an d Residues 26-35 are the exonic sequence.
<400> SEQUENCE: 86
E--> **cat ggc tga cct tct ccc tgg gca gga gaa gcc rt**
35
<210> SEQ ID NO: 87
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: exon
<222> LOCATION: (1)..(35)
<223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence and Resi dues 11-35 are the intronic sequence
<400> SEQUENCE: 87
E--> **cac cac cca ggt gcg cgg ggc tgc agg ggc gga ca**
35
<210> SEQ ID NO: 88
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: exon
<222> LOCATION: (1)..(35)
<223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic sequence an d Residues 26-35 are the exonic sequence.

RAW SEQUENCE LISTING DATE: 01/07/2003
PATENT APPLICATION: US/09/765,061C TIME: 14:04:21

Input Set : A:\SQ 09765061.txt
Output Set: N:\CRF4\01072003\I765061C.raw

195 <400> SEQUENCE: 88
E--> 196 gct gga tgc tcc ctg ctc ccc aca ggc atc gtg aa
197 35

VERIFICATION SUMMARY DATE: 01/07/2003
PATENT APPLICATION: **US/09/765,061C** TIME: 14:04:22

Input Set : **A:\SQ 09765061.txt**
Output Set: **N:\CRF4\01072003\I765061C.raw**

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:34 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:34 SEQ:79
L:52 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:35 SEQ:80
L:70 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:35 SEQ:81
L:88 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:35 SEQ:82
L:106 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:35 SEQ:83
L:124 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:35 SEQ:84
L:142 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:35 SEQ:85
L:160 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:35 SEQ:86
L:178 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:35 SEQ:87
L:196 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:35 SEQ:88

INPUT SEQ: W:\Client Files\TUVW\UT HSC Houston \UTHou16\UTL\UTHou-16UTL 79-88.ST25.txt

GENERAL INFORMATION SECTION

3,<110> The Board of Regents of the University of Texas System
5,<120> MUTATIONS IN A NOVEL PHOTORECEPTOR-PINEAL GENE ON 17P CAUSE LEBER
6, CONGENITAL AMAUROSIS (LCA4)
8,<130> 96606/16UTL
10,<140> 09/765,061
11,<141> 2001-01-17
13,<150> 60/331362
14,<151> 2001-01-04
16,<160> 10 additional sequences, Seq. Nos. 79-88
18,<170> PatentIn version 3.2

ERRORED LINES SECTION

STATISTICS SUMMARY

Application Serial Number: 09/765,061
Alpha or Numeric or Xml: Numeric
Application Class:
Application File Date: 2001-01-17
Art Unit:
Software Application: PatentIN3.2
Total Number of Sequences: 10
Total Nucleotides: 349
Total Amino Acids: 0
Number of Errors: 0
Number of Warnings: 0
Number of Corrections: 0

PAGE: 1 ERROR LISTING DATE: 06/06/2003

PATENT APPLICATION TIME: 11:32:34

INPUT SEQ: W:\Client Files\TUVW\UT HSC Houston \UTHou16\UTL\UTHou-16UTL 79-88.ST25.txt